



SEQUENCE LISTING

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ChemoCentryx, Inc.

#16

<120> Inhibition of CMV Infection and Dissemination

<130> 019934-002510US

<140> US 09/944,049

<141> 2001-08-30

<150> US 60/229,365

<151> 2000-08-30

<160> 48

<170> PatentIn Ver. 2.1

<210> 1

<211> 1065

<212> DNA

<213> Human cytomegalovirus

<220>

<223> human cytomegalovirus (HCMV) Toledo strain open
reading frame US28 (AU4.1)

<220>

<221> CDS

<222> (1)..(1065)

<223> HCMV Toledo US28

<400> 1

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ggcggtgtct ttctgttcgg ttccatcgcc aacttcttgg tgatcttcac catcacctgg 180
cgacgtcgga ttcaatgctc cggcgatgtt tactttatca acctcgcggc cggcgatttg 240
ctttcggtt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300
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tttacacgg agattgcact cgatcgctac tacgctattt tttacatgag atatcgccct 420
gtaaaacagg cctgcctttt cagtatttt tggtgatct ttgccgtat catcgccatt 480
ccacattttta tggtggtgac caaaaaagac aatcaatgta tgaccgacta cgactactta 540
gaggtcagct acccgatcat cctcaacgta gaactcatgc tcggtgctt cgtgatcccg 600
ctcagtgta tcagctactg ctactaccgc atttccagaa tcgttgcggc gtctcagtcg 660
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tggctgccgt accacctaac gctgtttgtg gacacgttaa aactcctcaa atggatctcc 780
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gaactgcact gtctgctggc cgagttcgc cagcgactt tttcccgca tgtatcctgg 960
taccacagca tgagctttc gcgtcggagc tcggcagac gaagagagac atcttccgac 1020
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<210> 2

<211> 354

<212> PRT

<213> Human cytomegalovirus

<220>

<223> human cytomegalovirus (HCMV) Toledo strain open
reading frame US28 (AU4.1)

<400> 2

Met Thr Pro Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
1 5 10 15

Asp Glu Ala Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
20 25 30

Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
35 40 45

Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
50 55 60

Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
65 70 75 80

Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
85 90 95

Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
100 105 110

Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
115 120 125

Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
130 135 140

Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
145 150 155 160

Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
165 170 175

Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
180 185 190

Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
195 200 205

Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
210 215 220

Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
225 230 235 240

Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
245 250 255

Lys Trp Ile Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
260 265 270

Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
275 280 285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
290 295 300

Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
305 310 315 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
325 330 335

Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
340 345 350

Ile Pro

<210> 3
<211> 1065
<212> DNA
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) VHL/E strain open
reading frame US28

<220>
<221> CDS
<222> (1)...(1065)
<223> HCMV VHL/E US28

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ggcgttgcgtc ttcttcggg ttccatcgcc aacttctgg tgatcttcac catcacctgg 180
cgacgtcgga ttcaatgttc cggcgatgtt tactttatca acctcgcggc cgccgatttg 240
ctttcggtt gtacactacc tctgtggatg caatacctcc tagatcacaa ctccctagcc 300
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tttacacgg agattgcact cgatcgctac tacgctattt tttacatgag atatcggcct 420
gtaaaacagg cctgcctttt cagttttt tggtgatct ttgccgtat catcgccatt 480
ccacacttta tggtggtgac caaaaaagac aatcaatgtt tgaccgacta cgactactta 540
gaggtcagtt acccgatcat cctcaacgtt gaactcatgc tcgggtgcgtt cgtgatcccg 600
ctcagtgtca tcagctactg ctactaccgc atttccagaa tcggtgcgtt gtctcagtcg 660
cgccacaaag gcccattgtt acgggtactt atagcggtcg tgcttgcgtt tatcatcttt 720
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taccacagca tgagcttttgc gctcggttgc tcggccgagcc gaagagagac gtcttccgac 1020
acgctgtccg acgaggcgttca caaattatac cgtaa 1065

<210> 4
<211> 354
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) VHL/E strain open
reading frame US28

<400> 4
Met Thr Pro Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
1 5 10 15

Asp Asp Glu Ala Thr Pro Cys Val Leu Thr Asp Val Leu Asn Gln Ser
 20 25 30

Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
 35 40 45

Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
 50 55 60

Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
 65 70 75 80

Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
 85 90 95

Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
 100 105 110

Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
 115 120 125

Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
 130 135 140

Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
 145 150 155 160

Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
 165 170 175

Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
 180 185 190

Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
 195 200 205

Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
 210 215 220

Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
 225 230 235 240

Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
 245 250 255

Lys Trp Ile Ser Ser Cys Glu Phe Glu Lys Ser Leu Lys Arg Ala
 260 265 270

Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
 275 280 285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
 290 295 300

Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
 305 310 315 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
 325 330 335

Thr Ser Ser Asp Thr Leu Ser Asp Glu Ala Cys Arg Val Ser Gln Ile
340 345 350

Ile Pro

<210> 5
<211> 1020
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.1

<220>
<221> CDS
<222> (1)...(1020)
<223> rhUS28.1

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tgcattatgtgt tagtcaagaa acgcaaactg cgtatccca gcgatgttta tttttccac 180
gcctctatgg ccgacactcgat cagcactgtc atgctaccgc tctggctaca ttatgtcctc 240
aactttgcc aactctctcg aggagcctgt atcagctttt cggtaactttt ctatgttccc 300
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tggatggcac ccattagcgt taagacggcc tttaaacact gcataggAAC ctggatcgta 420
tctgccttcg tggcatcacc ctactacgca tacagaaact cacacgacga acacgaatgc 480
attcttaggaa actacacttg gcacattaaac gaaccgctac acacgtgtat ggatgtgggt 540
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agacgaacga cctggggcaa tacttaggtt aacgaaaaga acagcgacat tcttatacgta 660
ctagttgtca tgacagtgtt ctttgggga ccgtttaata tcgtgttgggt tattgacaat 720
attttacaga gatactatga taccacgaat tgcgatgttag aaaagattaa acatatcatg 780
gctatgatct cagaagccat tggttattt cgcggattt cagcacctat tatttatacgta 840
gggatttagtg gcagatttcg cgaagagatt tactctctgt ttagacgcca gccgtataac 900
gatttggacc ccgatgccaa tcaattcatg attgaactca cttagccaggg aagaagtaga 960
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<210> 6
<211> 339
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.1

<400> 6
Met Asn Asn Thr Ser Cys Asn Phe Asn Val Thr Leu Asn Ala Ser Ala
1 5 10 15

Pro Ser Arg Tyr Ile Ala Ile Ala Met Tyr Ser Ile Val Ile Cys Ile
20 25 30

Gly Leu Val Gly Asn Leu Leu Leu Cys Ile Val Leu Val Lys Lys Arg
35 40 45

Lys Leu Arg Tyr Ser Ser Asp Val Tyr Phe Phe His Ala Ser Met Ala
50 55 60

Asp Leu Val Ser Thr Val Met Leu Pro Leu Trp Leu His Tyr Val Leu
 65 70 75 80
 Asn Phe Ala Gln Leu Ser Arg Gly Ala Cys Ile Ser Phe Ser Val Thr
 85 90 95
 Phe Tyr Val Pro Leu Phe Val Gln Ala Trp Leu Leu Ile Ser Ile Ala
 100 105 110
 Met Glu Arg Tyr Ser Asn Leu Val Trp Met Ala Pro Ile Ser Val Lys
 115 120 125
 Thr Ala Phe Lys His Cys Ile Gly Thr Trp Ile Val Ser Ala Phe Val
 130 135 140
 Ala Ser Pro Tyr Tyr Ala Tyr Arg Asn Ser His Asp Glu His Glu Cys
 145 150 155 160
 Ile Leu Gly Asn Tyr Thr Trp His Ile Asn Glu Pro Leu His Thr Cys
 165 170 175
 Met Asp Val Val Ile Ile Val Trp Thr Phe Leu Ala Pro Val Leu Val
 180 185 190
 Thr Ile Ile Ala Ser Val Lys Met Arg Arg Thr Thr Trp Gly Asn Thr
 195 200 205
 Arg Leu Asn Glu Lys Asn Ser Asp Ile Leu Ile Val Leu Val Val Met
 210 215 220
 Thr Val Phe Phe Trp Gly Pro Phe Asn Ile Val Leu Val Ile Asp Asn
 225 230 235 240
 Ile Leu Gln Arg Tyr Tyr Asp Thr Thr Asn Cys Asp Val Glu Lys Ile
 245 250 255
 Lys His Ile Met Ala Met Ile Ser Glu Ala Ile Val Tyr Phe Arg Gly
 260 265 270
 Ile Thr Ala Pro Ile Ile Tyr Val Gly Ile Ser Gly Arg Phe Arg Glu
 275 280 285
 Glu Ile Tyr Ser Leu Phe Arg Arg Gln Pro Tyr Asn Asp Leu Asp Pro
 290 295 300
 Asp Ala Asn Gln Phe Met Ile Glu Leu Thr Ser Gln Gly Arg Ser Arg
 305 310 315 320
 Asn Arg Asn Ala Arg Gln Ser Glu Ser Asn Val Pro Gln Pro Glu Glu
 325 330 335
 Cys Phe Trp

<210> 7
 <211> 1002
 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.2

<220>
<221> CDS
<222> (1)..(1002)
<223> rhUS28.2

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atactttgg ttttggcac gagacgcata cactggtcg caaatgacat ctactatctc 180
aacatgtat ttacagactt ttttgcattc attacattac ccgcctgggt ttactacctg 240
ctgaattaca cacaactctc acactatgcc tgcattgctc tatcattgt ttttacgtt 300
tccatTTTA ttcaagctga ctttatggta gcagtggcta tcgagcgtta tcgaaggcta 360
gtgaaaaaaca aacccttag cgtaaaaaaa gccagcgtca gctgcgcgtg catctggatc 420
atgttttata tagtgttctc accatactac atgttttagat cgcaacacga aacaaattct 480
tgcattctag gaaactacac ctggcatatg aacagtccctt ttgcgcacac aatggacgca 540
tccattaaca tttggcttt tgcgttccg gccgtacga cttgttaat agccagacga 600
atttatgtat gtacttcagg caacaaaaaa atgaacgcga gagccagtgg tttgttagag 660
gccatggta ttagcatgtt attcttcgga ggactttca acctgaacat cttecgagac 720
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atgtgtgtga gtaccagatt ggcggcaagaa ataaaaatgtt tgtttatgcg aatacctt 900
gaaacactag atgcagaaca cgctaaactc atggtaatt taaaaaacag aatgcta 960
gtaccggatc ctaaacctcg tgaatatgaa tctgtgttat ag 1002

<210> 8
<211> 333
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.2

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Met Thr Asn Ala Gly His Cys His Ile Asn Glu Ser Leu Ala Ser Tyr
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Gly Ile Ala Pro Ala Ala Thr Ile Thr Leu Tyr Ser Ile Ala Gly Ile
20 25 30

Cys Gly Val Thr Gly Asn Leu Leu Ile Leu Leu Val Leu Phe Thr Arg
35 40 45

Arg Ile His Trp Phe Ala Asn Asp Ile Tyr Tyr Leu Asn Met Ile Phe
50 55 60

Thr Asp Phe Leu Val Phe Ile Thr Leu Pro Ala Trp Val Tyr Tyr Leu
65 70 75 80

Leu Asn Tyr Thr Gln Leu Ser His Tyr Ala Cys Ile Ala Leu Ser Phe
85 90 95

Val Phe Tyr Val Ser Ile Phe Ile Gln Ala Asp Phe Met Val Ala Val
100 105 110

Ala Ile Glu Arg Tyr Arg Ser Leu Val Lys Asn Lys Pro Leu Ser Val
 115 120 125
 Lys Lys Ala Ser Val Ser Cys Ala Cys Ile Trp Ile Ile Val Ile Ile
 130 135 140
 Val Ser Ser Pro Tyr Tyr Met Phe Arg Ser Gln His Glu Thr Asn Ser
 145 150 155 160
 Cys Ile Leu Gly Asn Tyr Thr Trp His Met Asn Ser Pro Phe Arg Thr
 165 170 175
 Thr Met Asp Ala Ser Ile Asn Ile Trp Ser Phe Val Val Pro Ala Val
 180 185 190
 Thr Thr Leu Leu Ile Ala Arg Arg Ile Tyr Val Cys Thr Ser Gly Asn
 195 200 205
 Lys Lys Met Asn Ala Arg Ala Ser Gly Leu Leu Glu Ala Met Val Ile
 210 215 220
 Ser Met Leu Phe Phe Gly Gly Leu Phe Asn Leu Asn Ile Phe Arg Asp
 225 230 235 240
 Ile Val Ser Asp Thr Ser Glu Asp Asn Lys Asp Cys Thr Tyr Leu Lys
 245 250 255
 Gln Glu His Phe Ile Arg Met Val Gly Val Ala Leu Val Tyr Gly Arg
 260 265 270
 Ala Ile Phe Asn Pro Phe Met Tyr Met Cys Val Ser Thr Arg Leu Arg
 275 280 285
 Gln Glu Ile Lys Cys Leu Phe Met Arg Ile Pro Tyr Glu Thr Leu Asp
 290 295 300
 Ala Glu His Ala Lys Leu Met Val Asn Leu Lys Asn Arg Asn Ala Asn
 305 310 315 320
 Val Pro Asp Pro Lys Pro Arg Glu Tyr Glu Ser Val Leu
 325 330

<210> 9
 <211> 1014
 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.3

<220>
 <221> CDS
 <222> (1)..(1014)
 <223> rhUS28.3

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 attgtgctgc tcagcgtgct cgtcgtgaaa cgcaagctca agtttccgaa tgacattac 180

ttttcaacg cgtcttggc agacgtttt gccgtctgca tggtgcccgc ctgggttaac 240
 tatgcactgg actccacaca acttagcaag ttctcatgta tcactttac gttgggttt 300
 tacgtctccc tggatccatcca ggcctggatg ctcattctgg tcaccctgga gcgatacgga 360
 tctctagtct ggatcgcccc gatcaccaga aacaaagcca tagcgaattg tgtactctt 420
 tgcttggttt ccatcttctt ggccgcaccc tactactctt ttagaaacga aagcaacgaa 480
 caccatgca tcatgagaaa ctatacctgg agcgttggg aaacatggca catagccctg 540
 gatttcttaa ttacgctcat tacatttac atgcccagtga ctattgtgtt agctctgagt 600
 ttcaaaatgg ccagatggtc aacctttgg tacagaaacc tcaccaggag aaccagtctt 660
 atccttattt tgatactgac agtagcagca ggggtctggg gacctttca cctattttag 720
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 ctcagacact tgttagctt gatgaccgaa accctagtgt ttctacgttc agtttttaac 840
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 cgtactcagt atgatgctt ggacacgact cagttagcag aaactatgca gctgaaagcg 960
 aaagggtgtgc cgggtccga ccccgccg catgactgcg aatgctttt gtaa 1014

<210> 10

<211> 337

<212> PRT

<213> Rhesus cytomegalovirus

<220>

<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.3

<400> 10

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			20						25						30

Val	Val	Ile	Gly	Leu	Leu	Gly	Asn	Ile	Val	Leu	Leu	Ser	Val	Leu	Val
35							40								45

Val	Lys	Arg	Lys	Leu	Lys	Phe	Pro	Asn	Asp	Ile	Tyr	Phe	Phe	Asn	Ala
50						55					60				

Ser	Leu	Ala	Asp	Val	Phe	Ala	Val	Cys	Met	Leu	Pro	Ala	Trp	Val	Asn
65						70				75					80

Tyr	Ala	Leu	Asp	Ser	Thr	Gln	Leu	Ser	Lys	Phe	Ser	Cys	Ile	Thr	Phe
85							90								95

Thr	Phe	Gly	Phe	Tyr	Val	Ser	Leu	Phe	Ile	Gln	Ala	Trp	Met	Leu	Ile
100							105								110

Leu	Val	Thr	Leu	Glu	Arg	Tyr	Gly	Ser	Leu	Val	Trp	Ile	Ala	Pro	Ile
115							120								125

Thr	Arg	Asn	Lys	Ala	Ile	Ala	Asn	Cys	Val	Leu	Phe	Trp	Leu	Val	Ser
130							135								140

Ile	Phe	Leu	Ala	Ala	Pro	Tyr	Tyr	Ser	Phe	Arg	Asn	Glu	Ser	Asn	Glu
145						150				155					160

His	Gln	Cys	Ile	Met	Arg	Asn	Tyr	Thr	Trp	Ser	Val	Gly	Glu	Thr	Trp
165							170							175	

His	Ile	Ala	Leu	Asp	Phe	Leu	Ile	Thr	Leu	Ile	Thr	Phe	Ile	Met	Pro
180							185							190	

Val Thr Ile Val Leu Ala Leu Ser Phe Lys Met Ala Arg Trp Ser Thr
195 200 205

Phe Gly Tyr Arg Asn Leu Thr Ser Arg Thr Ser Leu Ile Leu Ile Leu
210 215 220

Ile Leu Thr Val Ala Ala Gly Phe Trp Gly Pro Phe His Leu Phe Met
225 230 235 240

Phe Ile Glu Asn Val Ala Gly Gln Ile Tyr His Ile Gln Lys Asp Cys
245 250 255

Trp Tyr Leu Gln Leu Arg His Leu Cys Ser Leu Met Thr Glu Thr Leu
260 265 270

Val Phe Leu Arg Ser Val Phe Asn Pro Tyr Ile Tyr Met Ile Ile Ser
275 280 285

Tyr Lys Phe Arg Gln Gln Val Arg Ser Leu Leu Lys Arg Thr Gln Tyr
290 295 300

Asp Ala Leu Asp Thr Thr Gln Leu Ala Glu Thr Met Gln Leu Lys Ala
305 310 315 320

Lys Gly Val Pro Val Ser Asp Pro Ala Pro His Asp Cys Glu Cys Phe
325 330 335

Leu

<210> 11
<211> 987
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.4

<220>
<221> CDS
<222> (1)...(987)
<223> rhUS28.4

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aaccatcaga gacgacacccg gacaaacagt ttcagtgtatg ttttatttcg acatctcatg 180
atcacccgaag aggtctttac cctcaccatt cccgtctggg cgtatcaactt aactactcac 240
ggcaacttac cgggctcggt gtgccgaagt ctcacccctcg ttttttatct aacggatttc 300
gctcgtgcct tcttttacct gtcctcatac tgggaccgat acagcgtaat catctgcaga 360
caccctctcc ccgttaatct gaactacagt caggtcatag gcctgtctgt ctggctgggt 420
gccgtactgt cagcatcacc gttctccatt tttaacggaa gtgtgaaaca atgcctgggc 480
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tccttctgggt taccgctcat catgtcggt aactgttact accaagaaaa acggccgagca 600
tcgcctgacc aactccacga actttaccga tgcagttgc taattaccat tatcacaact 660
tacgctatcg tatgggttcc tttccatctc gctttactca tagacccct gattagcata 720
agccatgttag aaccctcttag cgctctccac tgggcatcca ttgtcgttac ctgtaaatca 780
tttacatttg tatatgcggg cataagccca cttagtgtatt tcacatgctg ccccaccgta 840
cgtcgcgaac tgctgatgtc tctacgtcca ttcttcaccc ggattttccag caaaacgcgg 900
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<210> 12
 <211> 328
 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.4

<400> 12
 Met Asn Ser Ser Gln His Asn Ile Ser Val Phe Leu Ser Ile Gly Ala
 1 5 10 15
 Gly Pro Val Ile Thr Gly Tyr Thr Cys Val Phe Leu Phe Gly Ile Leu
 20 25 30
 Gly His Phe Tyr Leu Tyr Trp Lys Asn His Gln Arg Arg His Arg Thr
 35 40 45
 Asn Ser Phe Ser Asp Val Leu Phe Arg His Leu Met Ile Thr Glu Glu
 50 55 60
 Val Phe Thr Leu Thr Ile Pro Val Trp Ala Tyr His Leu Thr Thr His
 65 70 75 80
 Gly Asn Leu Pro Gly Ser Trp Cys Arg Ser Leu Thr Phe Val Phe Tyr
 85 90 95
 Leu Thr Val Phe Ala Arg Ala Phe Phe Tyr Leu Leu Leu Ile Trp Asp
 100 105 110
 Arg Tyr Ser Val Ile Ile Cys Arg His Pro Leu Pro Val Asn Leu Asn
 115 120 125
 Tyr Ser Gln Val Ile Gly Leu Ser Val Trp Leu Val Ala Val Leu Ser
 130 135 140
 Ala Ser Pro Phe Ser Ile Phe Asn Gly Ser Val Lys Gln Cys Leu Gly
 145 150 155 160
 Asn Met Gly Ser Ile Pro Ser Glu Ser Ser Ala Val Leu Asn Leu Glu
 165 170 175
 Val His Leu Cys Ser Phe Trp Leu Pro Leu Ile Met Ser Ala Asn Cys
 180 185 190
 Tyr Tyr Gln Ala Lys Arg Arg Ala Ser Pro Asp Gln Leu His Glu Leu
 195 200 205
 Tyr Arg Cys Ser Leu Leu Ile Thr Ile Ile Thr Thr Tyr Ala Ile Val
 210 215 220
 Trp Phe Pro Phe His Leu Ala Leu Leu Ile Asp Ala Leu Ile Ser Ile
 225 230 235 240
 Ser His Val Glu Pro Ser Ser Ala Leu His Trp Ala Ser Ile Val Val
 245 250 255

Thr Cys Lys Ser Phe Thr Phe Val Tyr Ala Gly Ile Ser Pro Leu Val
260 265 270

Tyr Phe Thr Cys Cys Pro Thr Val Arg Arg Glu Leu Leu Met Ser Leu
275 280 285

Arg Pro Phe Phe Thr Trp Ile Ser Ser Lys Thr Arg Arg Gly Tyr Ala
290 295 300

Pro Ile Lys Thr Gln Pro Leu Asn Ile Pro Asp Glu Pro Ile Asp Asn
305 310 315 320

Lys Ser Pro His Leu Leu Asn Glu
325

<210> 13

<211> 1452

<212> DNA

<213> Rhesus cytomegalovirus

<220>

<223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
rhUS28.5

<220>

<221> CDS

<222> (1)..(1452)

<223> rhUS28.5

<400> 13

atgactacca ccacaatgag tgctaccacg aattccagta ccacgcctca agcaagcagc 60
accacgatga caacgaagac aagcactcct ggcaatacaa ctactggcac tacgtccacc 120
ctgacaacga tatcaacaac ttctaatgct accagcataa cgtctaattt aagcactacc 180
ggaaacccaaa ctgcaactac caatgctact accttcagtt ccacattaac aacatctaca 240
aatataagca gtacatttc gacagtttct accgtcgcat ccaatgcaac atgtaattct 300
acaatcacaa cgaatattac aactgctttt actacagcag caaacactac cgcaagcagc 360
ctcaccagca tcgtaacttc acttgccact accattgaaa ccacatcatt tgattatgat 420
gagtcagcag aagcttgcaa cttAACAGAC atcgttcata ctactagatc agtgacagtt 480
actttctata ctatcatatt catactccgc ctttggaa actttctggc tcttatgacc 540
atcatttgga accgtcgcat ttcctttatg gttgaaatat atttcgtaa tctagcaatc 600
tccgatctta tgTTTGTATG tactttacca tttggataa tgtatcttct tgagcacgac 660
gtcatgtcac atgcattctg tgtagcaatg acagccattt tttattgcgc gctgtttgcc 720
agcaactgttt tcctcttgct aattgtttt gacagatgtt acgctattct attaggtaca 780
gaaaaagcaa atagacgttt attgcgcaat gctgtttctg gatgcgtct catgtgggaa 840
ttgtgtttca ttttagcatt acctcattt atctttatga agaaaagaac caacgtatgt 900
gtagcagagt atgaaccagg acttaacaat ttctatgtt ttttatcaa tactgaggtg 960
aacctatgca ccctagttt gccagccgca gcccattatct actggtatct taaactaacc 1020
aaagcactca aaacccatga acgactgcgt cataggctaa cgtctctaaa catagtgtt 1080
gctgttgtca ttgttattgc tttgtttgg ctggcgata atctcatgtc tatgtatgtat 1140
agcttagttc acatgcagat accttggaa tgcagctctg aaaaaataact gagacgaagt 1200
ttaattatta cagaatccat cggcctcagt cactgttgca tcaacccat tatctacttg 1260
ctcttcggac ctcgcgtgtc aagcgagttc tgcacgtgt tgcgatgtt cttacgcgc 1320
ttatgtccac acagatcctg gagttccata cgtcagaga cggtgccat cagtctcagt 1380
cactcacagg tatctgcattc atctgaggat gatgacaacg atgtgcattga tgaattgcaa 1440
tttttaattt ga 1452

<210> 14
 <211> 483
 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) US28 homolog
 rhUS28.5

<400> 14
 Met Thr Thr Thr Met Ser Ala Thr Thr Asn Ser Ser Thr Thr Pro
 1 5 10 15

Gln Ala Ser Ser Thr Thr Met Thr Thr Lys Thr Ser Thr Pro Gly Asn
 20 25 30

Thr Thr Thr Gly Thr Thr Ser Thr Leu Thr Thr Ile Ser Thr Thr Ser
 35 40 45

Asn Ala Thr Ser Ile Thr Ser Asn Leu Ser Thr Thr Gly Asn Gln Thr
 50 55 60

Ala Thr Thr Asn Ala Thr Thr Phe Ser Ser Thr Leu Thr Thr Ser Thr
 65 70 75 80

Asn Ile Ser Ser Thr Phe Ser Thr Val Ser Thr Val Ala Ser Asn Ala
 85 90 95

Thr Cys Asn Ser Thr Ile Thr Thr Asn Ile Thr Thr Ala Phe Thr Thr
 100 105 110

Ala Ala Asn Thr Thr Ala Ser Ser Leu Thr Ser Ile Val Thr Ser Leu
 115 120 125

Ala Thr Thr Ile Glu Thr Thr Ser Phe Asp Tyr Asp Glu Ser Ala Glu
 130 135 140

Ala Cys Asn Leu Thr Asp Ile Val His Thr Thr Arg Ser Val Thr Val
 145 150 155 160

Thr Phe Tyr Thr Ile Ile Phe Ile Leu Gly Leu Leu Gly Asn Phe Leu
 165 170 175

Val Leu Met Thr Ile Ile Trp Asn Arg Arg Ile Ser Phe Met Val Glu
 180 185 190

Ile Tyr Phe Val Asn Leu Ala Ile Ser Asp Leu Met Phe Val Cys Thr
 195 200 205

Leu Pro Phe Trp Ile Met Tyr Leu Leu Glu His Asp Val Met Ser His
 210 215 220

Ala Ser Cys Val Ala Met Thr Ala Ile Phe Tyr Cys Ala Leu Phe Ala
 225 230 235 240

Ser Thr Val Phe Leu Leu Ile Val Leu Asp Arg Cys Tyr Ala Ile
 245 250 255

Leu Leu Gly Thr Glu Lys Ala Asn Arg Arg Leu Leu Arg Asn Ala Val
 260 265 270

Ser Gly Cys Met Leu Met Trp Gly Leu Cys Phe Ile Leu Ala Leu Pro
 275 280 285
 His Phe Ile Phe Met Lys Lys Gly Thr Asn Val Cys Val Ala Glu Tyr
 290 295 300
 Glu Pro Gly Leu Asn Asn Phe Tyr Val Ile Phe Ile Asn Thr Glu Val
 305 310 315 320
 Asn Leu Cys Thr Leu Val Leu Pro Ala Ala Ala Ile Ile Tyr Trp Tyr
 325 330 335
 Leu Lys Leu Thr Lys Ala Leu Lys Thr His Glu Arg Leu Arg His Arg
 340 345 350
 Leu Thr Ser Leu Asn Ile Val Leu Ala Val Val Ile Val Phe Ala Leu
 355 360 365
 Phe Trp Leu Pro Tyr Asn Leu Met Leu Met Met Tyr Ser Leu Val His
 370 375 380
 Met Gln Ile Pro Trp Glu Cys Ser Ser Glu Lys Ile Leu Arg Arg Ser
 385 390 395 400
 Leu Ile Ile Thr Glu Ser Ile Ala Leu Ser His Cys Cys Ile Asn Pro
 405 410 415
 Ile Ile Tyr Leu Leu Phe Gly Pro Arg Cys Arg Ser Glu Phe Cys His
 420 425 430
 Leu Leu Arg Cys Cys Phe Thr Arg Leu Cys Pro His Arg Ser Trp Ser
 435 440 445
 Ser Ile Arg Ala Glu Thr Val Ser Ile Ser Leu Ser His Ser Gln Val
 450 455 460
 Ser Ala Ser Ser Glu Asp Asp Asp Asn Asp Val His Asp Glu Leu Gln
 465 470 475 480
 Phe Leu Ile

<210> 15
 <211> 1296
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL78

<220>
 <221> CDS
 <222> (1)...(1296)
 <223> HCMV AD169 UL78

<400> 15
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 agtttcaaac acatgggccc gttcgaaggc tactctatgt cggccgatcg cgccgcctcg 120
 gatctactca tcggcatgtt cggctccgtt agcctggtca acctgctgac tatcatcggt 180
 tgcctctggg tggcgtgt tacgcggccg cccgtgtccg tggatgttt tacttggaaat 240

ctggtaactta gtcagttttt ttccatcctg gccaccatgt tgcgtccaaaggg tatcatgctg 300
 cgtggcgctc taaatctcag cctctgtcgc tttagtgcctt ttgtgcacga cgtggggccta 360
 tattcgacgg cgttttttt cctcttctg atactggatc gtctgtccgc catatcttac 420
 ggcgcgtgatc tctggcatca tgagacgcgc gaaaacgcgc ggcgtggcgct ctacgcggtc 480
 gccttcgcct gggttcttc catcgtagcc gctgtgccta cgcgcctac gggttactg 540
 gactaccgtt ggcttaggctg tcagatccct atacagtatg cgcgggtgga cctcaccatc 600
 aagatgtggt ttttgcgtgg ggcgcctatg atgcgcgtac tggctaacgt ggttagagttg 660
 gcctacagcg atcggcgcgca ccacgtctgg tcctacgtgg gtcgtgtctg caccttctac 720
 gtgacgtgtc tcatgtctt tgcgtccctac tactgttca gagtcctacg cgtgtactg 780
 cagcccccta ggcggccgg caccggttt ggcattatgg attacgtgga attggctacg 840
 cgtacccttc tcaccatgcg tcttggcatt ctggcgctct ttatcattgc gtcttctcc 900
 cgcgagccca ccaaggatct ggttgcactcc ttgttattatc tggtcgagag atgtcagcaa 960
 agctgccacg gtcatttcgt acgtcggtt gtcaggcggt tgaagcgggc tatgtatagc 1020
 gtggagctgg cctgtgttta cttttctacg tccgtccgag acgtcgccga ggcggtgaaa 1080
 aagtccctcca gccgtgttta cgccgacgcg acgtcgccgg ccgttgcgtt aacgacaacc 1140
 acgtcgagaga aagccacgtt ggttgcgtt gccgaaaggca tggcttccga aatgtgtccct 1200
 gggactacga tcgtatgttcc ggcgaaagt tcctccgtcc tctgcaccga cggcgaaaac 1260
 accgtcgcggtt cggacgcgac ggtgacggca ttatga 1296

<210> 16
 <211> 431
 <212> PRT
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL78

<400> 16
 Met Ser Pro Ser Val Glu Glu Thr Thr Ser Val Thr Glu Ser Ile Met
 1 5 10 15

Phe Ala Ile Val Ser Phe Lys His Met Gly Pro Phe Glu Gly Tyr Ser
 20 25 30

Met Ser Ala Asp Arg Ala Ala Ser Asp Leu Leu Ile Gly Met Phe Gly
 35 40 45

Ser Val Ser Leu Val Asn Leu Leu Thr Ile Ile Gly Cys Leu Trp Val
 50 55 60

Leu Arg Val Thr Arg Pro Pro Val Ser Val Met Ile Phe Thr Trp Asn
 65 70 75 80

Leu Val Leu Ser Gln Phe Phe Ser Ile Leu Ala Thr Met Leu Ser Lys
 85 90 95

Gly Ile Met Leu Arg Gly Ala Leu Asn Leu Ser Leu Cys Arg Leu Val
 100 105 110

Leu Phe Val Asp Asp Val Gly Leu Tyr Ser Thr Ala Leu Phe Phe Leu
 115 120 125

Phe Leu Ile Leu Asp Arg Leu Ser Ala Ile Ser Tyr Gly Arg Asp Leu
 130 135 140

Trp His His Glu Thr Arg Glu Asn Ala Gly Val Ala Leu Tyr Ala Val
 145 150 155 160

Ala Phe Ala Trp Val Leu Ser Ile Val Ala Ala Val Pro Thr Ala Ala
 165 170 175
 Thr Gly Ser Leu Asp Tyr Arg Trp Leu Gly Cys Gln Ile Pro Ile Gln
 180 185 190
 Tyr Ala Ala Val Asp Leu Thr Ile Lys Met Trp Phe Leu Leu Gly Ala
 195 200 205
 Pro Met Ile Ala Val Leu Ala Asn Val Val Glu Leu Ala Tyr Ser Asp
 210 215 220
 Arg Arg Asp His Val Trp Ser Tyr Val Gly Arg Val Cys Thr Phe Tyr
 225 230 235 240
 Val Thr Cys Leu Met Leu Phe Val Pro Tyr Tyr Cys Phe Arg Val Leu
 245 250 255
 Arg Gly Val Leu Gln Pro Ala Ser Ala Ala Gly Thr Gly Phe Gly Ile
 260 265 270
 Met Asp Tyr Val Glu Leu Ala Thr Arg Thr Leu Leu Thr Met Arg Leu
 275 280 285
 Gly Ile Leu Pro Leu Phe Ile Ile Ala Phe Phe Ser Arg Glu Pro Thr
 290 295 300
 Lys Asp Leu Asp Asp Ser Phe Asp Tyr Leu Val Glu Arg Cys Gln Gln
 305 310 315 320
 Ser Cys His Gly His Phe Val Arg Arg Leu Val Gln Ala Leu Lys Arg
 325 330 335
 Ala Met Tyr Ser Val Glu Leu Ala Val Cys Tyr Phe Ser Thr Ser Val
 340 345 350
 Arg Asp Val Ala Glu Ala Val Lys Lys Ser Ser Arg Cys Tyr Ala
 355 360 365
 Asp Ala Thr Ser Ala Ala Val Val Val Thr Thr Thr Ser Glu Lys
 370 375 380
 Ala Thr Leu Val Glu His Ala Glu Gly Met Ala Ser Glu Met Cys Pro
 385 390 395 400
 Gly Thr Thr Ile Asp Val Ser Ala Glu Ser Ser Ser Val Leu Cys Thr
 405 410 415
 Asp Gly Glu Asn Thr Val Ala Ser Asp Ala Thr Val Thr Ala Leu
 420 425 430

<210> 17
 <211> 1140
 <212> DNA
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL78 homolog
 (rhUL78)

<220>
<221> CDS
<222> (1)..(1140)
<223> rhUL78

<400> 17
atgattacgg agcgcgtcct cgcaaggcatc ctcgcggca tgacggccgc ggggagttt 60
gtcattctcc tcgcgggtgt tatgtgggtg aacatgttag atcgcgtgg catgccaatg 120
gccgttgggc attacacagg gaacctgggtg ttgactcagg tcatactgtat cttctccatg 180
ctggcgctcta aaattgttgg catgacgagt gcccaca tgggctctg cgccatcg 240
gttttctgg aagacactgg cctctatgtc acctcgctgc tcttcatgtt tatgatcctg 300
gatcgcatgg cggctttct taacgggctt ctttctgg agcagcagac gacgaagcag 360
aatctgagta caagcgtgta cattattctg ttttctggg tggtggaaat ggccgcggct 420
gttcccagcg cggctgtggc tgcacccaat tccaggtggg aacgctgcga aattccagtg 480
tcatatgccg caatcgacat gattgtgaag ctctgggtt tgctgtggc acccgctgtg 540
ctgattatgg ctgtgatcat tcaatcttc tatacatcg 600
tatgccagac gtgtgttcat gttctacacg gcctgttttgc tcatgatggt gccttattac 660
ttcgtcagag tcatgctgag cgactttgtt ttgggtgata taaaaacaaa aacggcgaac 720
agcgacggtt gtgattcgac atttcttgat tatactgaaca tgttcaactca cgtgatttac 780
agtttaagt tgggtgggtt tgctttgtt attgtcctgt tttgctccat aaacccgatg 840
gaaacgctgg aagaatgctt ggagaggccc gatgctgaga ggcaaagtgc gtcagaagca 900
tcccagggtt aaaggaggct gccaatcaac acatgctgta taaagtgtat tgaattgata 960
aagcagtatg taagcactct ctctaaagcc acgagggaca attctggcga aagggccaat 1020
ttgccagaga atgctgaaga tattggaaaca actggcagtg atcagctacc gactgaggc 1080
accgtgaccc caaattcattc ggctgtgtt agcactggag gaacgggtgc tccagtctaa 1140

<210> 18
<211> 379
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL78 homolog
(rhUL78)

<400> 18
Met Ile Thr Glu Arg Val Leu Ala Gly Ile Leu Ala Gly Met Thr Ala
1 5 10 15

Ala Gly Ser Leu Val Ile Leu Leu Ala Val Val Met Trp Leu Asn Met
20 25 30

Leu Asp Arg Ala Gly Met Pro Met Ala Val Gly His Tyr Thr Gly Asn
35 40 45

Leu Val Leu Thr Gln Val Ile Cys Ile Phe Ser Met Leu Ala Ser Lys
50 55 60

Ile Val Gly Met Thr Ser Ala Ala Asn Met Gly Phe Cys Gly Ile Val
65 70 75 80

Val Phe Leu Glu Asp Thr Gly Leu Tyr Val Thr Ser Leu Leu Phe Met
85 90 95

Phe Met Ile Leu Asp Arg Met Ala Ala Phe Leu Asn Gly Arg Leu Phe
100 105 110

Trp Arg Gln Gln Thr Thr Lys Gln Asn Leu Ser Thr Ser Val Tyr Ile
115 120 125

Ile Leu Phe Cys Trp Val Leu Gly Met Ala Ala Ala Val Pro Ser Ala
 130 135 140
 Ala Val Ala Ala Pro Asn Ser Arg Trp Glu Arg Cys Glu Ile Pro Val
 145 150 155 160
 Ser Tyr Ala Ala Ile Asp Met Ile Val Lys Leu Trp Phe Val Leu Leu
 165 170 175
 Ala Pro Val Val Leu Ile Met Ala Val Ile Ile Gln Ser Ser Tyr His
 180 185 190
 Arg Asp Arg Glu Arg Ile Trp Tyr Tyr Ala Arg Arg Val Phe Met Phe
 195 200 205
 Tyr Thr Ala Cys Phe Val Met Met Val Pro Tyr Tyr Phe Val Arg Val
 210 215 220
 Met Leu Ser Asp Phe Ala Leu Val Asp Ile Lys Thr Lys Thr Ala Asn
 225 230 235 240
 Ser Asp Gly Cys Asp Ser Thr Phe Leu Asp Tyr Leu Asn Met Phe Thr
 245 250 255
 His Val Ile Tyr Ser Phe Lys Leu Val Val Phe Ala Leu Phe Ile Val
 260 265 270
 Leu Phe Cys Ser Ile Asn Pro Met Glu Thr Leu Glu Glu Cys Leu Glu
 275 280 285
 Arg Ala Asp Ala Glu Arg Gln Ser Arg Ser Glu Ala Ser Gln Gly Glu
 290 295 300
 Arg Arg Leu Pro Ile Asn Thr Cys Cys Ile Lys Leu Ile Glu Leu Ile
 305 310 315 320
 Lys Gln Tyr Val Ser Thr Leu Ser Lys Ala Thr Arg Asp Asn Ser Gly
 325 330 335
 Glu Arg Ala Asn Leu Pro Glu Asn Ala Glu Asp Ile Gly Thr Thr Gly
 340 345 350
 Ser Asp Gln Leu Pro Thr Glu Val Thr Val Thr Pro Asn Ser Ser Ala
 355 360 365
 Val Phe Ser Thr Gly Gly Thr Val Ser Pro Val
 370 375

<210> 19
 <211> 1173
 <212> DNA
 <213> Human cytomegalovirus

 <220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL33

<220>
<221> CDS
<222> (1)..(1173)
<223> HCMV AD169 UL33

<400> 19
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ttcggtggcg gtccactaa cgccatagtg ttgatcacgc agctgctcac gaatcgcg 120
cttggctatt cgacgcccac catttacatg accaacctct actctactaa ttttctcacg 180
cttactgtgc taccctttat cgtactcagc aaccagtggc tggccggc cggcgtggc 240
tcgtgtaaat ttctatcggt gatctactac tcaagctgca cagtggc ttgcaccgta 300
gctctgatecg ccggccatcg ttatcgctc cttcataaac gaacatacgc acgccaatca 360
taccgttcaa cctatatgt tttgttattt acatggctcg ctggactaat ttttccgtg 420
cccgagctg tttacaccac ggtggatgatc catcacatg ccaacgatac caataatact 480
aatgggcacg ccacatgtgt actgtacttc gtagctgaag aagtgcacac agtgctgctt 540
tcgtggaaag tgctgctgac gatggatgg ggtggccac ccgtgataat gatgacgtgg 600
ttctacgcat tttctactc aaccgtacag cgacgtcac agaaacaaag gagtcgtacc 660
ttaacctttt ttagcgtgct actcatctcc ttctgtggc tacaaaactcc ctacgtctct 720
ctcatgatct tcaacagtta tgccacaacc gcctggccca tgcagtgtga acacactcaca 780
ctgcgacgca ccattggcac gctggcgctg gtggtgcaccc acctacactg cctcattaaat 840
cccatcctgt acgcgctgct gggcatgat tttctgcaac gcatgcccga gtgtttccgc 900
ggtcagttgc tggaccggccg cgctttctg agatcgacg agaatacgag agtacacg 960
gagacaaatc tagcggctgg caacaattca caatcagtgg ctacgtcatt agacaccaat 1020
agcaaaaact acaatcagca cgccaaacgc agcgtgtctt tcaattttcc cagcggtacg 1080
tgaaaaggcg gccagaaaac cgcgccaac gacacatcca caaaaatccc ccatcgactc 1140
tcacaatcgc atcataacct cagcgggta tga 1173

<210> 20
<211> 390
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL33

<400> 20
Met Thr Gly Pro Leu Phe Ala Ile Arg Thr Thr Glu Ala Val Leu Asn
1 5 10 15

Thr Phe Ile Ile Phe Val Gly Gly Pro Leu Asn Ala Ile Val Leu Ile
20 25 30

Thr Gln Leu Leu Thr Asn Arg Val Leu Gly Tyr Ser Thr Pro Thr Ile
35 40 45

Tyr Met Thr Asn Leu Tyr Ser Thr Asn Phe Leu Thr Leu Thr Val Leu
50 55 60

Pro Phe Ile Val Leu Ser Asn Gln Trp Leu Leu Pro Ala Gly Val Ala
65 70 75 80

Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr Ser Ser Cys Thr Val Gly
85 90 95

Phe Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Leu His
100 105 110

Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg Ser Thr Tyr Met Ile Leu
115 120 125

Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe Ser Val Pro Ala Ala Val
 130 135 140
 Tyr Thr Thr Val Val Met His His Asp Ala Asn Asp Thr Asn Asn Thr
 145 150 155 160
 Asn Gly His Ala Thr Cys Val Leu Tyr Phe Val Ala Glu Glu Val His
 165 170 175
 Thr Val Leu Leu Ser Trp Lys Val Leu Leu Thr Met Val Trp Gly Ala
 180 185 190
 Ala Pro Val Ile Met Met Thr Trp Phe Tyr Ala Phe Phe Tyr Ser Thr
 195 200 205
 Val Gln Arg Thr Ser Gln Lys Gln Arg Ser Arg Thr Leu Thr Phe Val
 210 215 220
 Ser Val Leu Leu Ile Ser Phe Val Ala Leu Gln Thr Pro Tyr Val Ser
 225 230 235 240
 Leu Met Ile Phe Asn Ser Tyr Ala Thr Thr Ala Trp Pro Met Gln Cys
 245 250 255
 Glu His Leu Thr Leu Arg Arg Thr Ile Gly Thr Leu Ala Arg Val Val
 260 265 270
 Pro His Leu His Cys Leu Ile Asn Pro Ile Leu Tyr Ala Leu Leu Gly
 275 280 285
 His Asp Phe Leu Gln Arg Met Arg Gln Cys Phe Arg Gly Gln Leu Leu
 290 295 300
 Asp Arg Arg Ala Phe Leu Arg Ser Gln Gln Asn Gln Arg Ala Thr Ala
 305 310 315 320
 Glu Thr Asn Leu Ala Ala Gly Asn Asn Ser Gln Ser Val Ala Thr Ser
 325 330 335
 Leu Asp Thr Asn Ser Lys Asn Tyr Asn Gln His Ala Lys Arg Ser Val
 340 345 350
 Ser Phe Asn Phe Pro Ser Gly Thr Trp Lys Gly Gly Gln Lys Thr Ala
 355 360 365
 Ser Asn Asp Thr Ser Thr Lys Ile Pro His Arg Leu Ser Gln Ser His
 370 375 380
 His Asn Leu Ser Gly Val
 385 390

<210> 21
 <211> 1239
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <223> human cytomegalovirus (HCMV) AD169 strain open
 reading frame UL33 splice variant (UL33 spliced)

<220>
<221> CDS
<222> (1)..(1239)
<223> HCMV AD169 UL33 spliced

<400> 21
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tgcaacatga cagggccgtt attcgcatt cgaaccacccg aagccgtact caacacattc 120
atcatcttcg tggcggtcc acttaacgcc atatgttgc tcacgcagct gctcacgaat 180
cgcgtgcttgcgtt getattcgac gcccaccatt tacatgacca acctctactc tactaatttt 240
ctcacgctta ctgtgttacc ctttatcgta ctcagcaacc agtggctgtt gccggccggc 300
gtggcctcggtt gtaaatttct atcgggtatc tactactcaa gctgcacagt gggctttgcc 360
accgttagtc tgatcgccgc cgatcgatc cgcgtcccccataaaacgaac atacgcacgc 420
caatcataacc gttcaaccta tatgattttg ctattgacat ggctcgctgg actaattttt 480
tccgtcccccg cagctgttta caccacggtg gtatgcattc acgatgcacaa cgataccaaat 540
aatactaattg ggcacgcccac ctgtgtactg tacttcgttag ctgaagaagt gcacacagt 600
ctgcttcgtt gggaaagtgtt gctgacgatg gtatgggttgc cgcacccgt gataatgtat 660
acgtgggttctt acgcatttctt ctactcaacc gtacagcgcacatcgacagagaa acaaaggagt 720
cgtaccttaa cctttgttag cgtgttactc atctccttcg tggcgcttaca aactccctac 780
gtctctctca tgatcttcaa cagttatgcc acaaccgcctt ggcccatgca gtgtgaacac 840
ctcacactgc gacgcacccat tggcacgttgcgcgtgttgc tgcccccacactgcctc 900
attaatccca tcctgtacgc gctgtgggtt catgattttc tgcaacgcacat gggcgagtgt 960
ttcccgccgttccatgttgcggaa cccggccgtt tcctgttagat cgcacgcacaaat tcagcgagct 1020
acagcggaga caaatcttagc ggctggcaac aattcacaat cagttgttac gtcatttagac 1080
accaatagca aaaactacaaatcagcacgc aacgcacgcg tgcgtttcaat tttcccaac 1140
ggtagtggaa aaggcgccca gaaaaccgcg tccaaacgcaca catccacaaa aatcccccat 1200
cgactctcacaatcgatca taacccatcgggtatga 1239

<210> 22
<211> 412
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame UL33 splice variant (UL33 spliced)

```

<400> 22
Met Asp Thr Ile Ile His Asn Ser Thr Arg Asn Asn Thr Pro Pro His
      1          5          10          15

Ile Asn Asp Thr Cys Asn Met Thr Gly Pro Leu Phe Ala Ile Arg Thr
      20          25          30

Thr Glu Ala Val Leu Asn Thr Phe Ile Ile Phe Val Gly Gly Pro Leu
      35          40          45

Asn Ala Ile Val Leu Ile Thr Gln Leu Leu Thr Asn Arg Val Leu Gly
      50          55          60

Tyr Ser Thr Pro Thr Ile Tyr Met Thr Asn Leu Tyr Ser Thr Asn Phe
      65          70          75          80

Leu Thr Leu Thr Val Leu Pro Phe Ile Val Leu Ser Asn Gln Trp Leu
      85          90          95

Leu Pro Ala Gly Val Ala Ser Cys Lys Phe Leu Ser Val Ile Tyr Tyr
      100         105         110

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Ser Ser Cys Thr Val Gly Phe Ala Thr Val Ala Leu Ile Ala Ala Asp
115 120 125

Arg Tyr Arg Val Leu His Lys Arg Thr Tyr Ala Arg Gln Ser Tyr Arg
130 135 140

Ser Thr Tyr Met Ile Leu Leu Thr Trp Leu Ala Gly Leu Ile Phe
145 150 155 160

Ser Val Pro Ala Ala Val Tyr Thr Thr Val Val Met His His Asp Ala
165 170 175

Asn Asp Thr Asn Asn Thr Asn Gly His Ala Thr Cys Val Leu Tyr Phe
180 185 190

Val Ala Glu Glu Val His Thr Val Leu Leu Ser Trp Lys Val Leu Leu
195 200 205

Thr Met Val Trp Gly Ala Ala Pro Val Ile Met Met Thr Trp Phe Tyr
210 215 220

Ala Phe Phe Tyr Ser Thr Val Gln Arg Thr Ser Gln Lys Gln Arg Ser
225 230 235 240

Arg Thr Leu Thr Phe Val Ser Val Leu Leu Ile Ser Phe Val Ala Leu
245 250 255

Gln Thr Pro Tyr Val Ser Leu Met Ile Phe Asn Ser Tyr Ala Thr Thr
260 265 270

Ala Trp Pro Met Gln Cys Glu His Leu Thr Leu Arg Arg Thr Ile Gly
275 280 285

Thr Leu Ala Arg Val Val Pro His Leu His Cys Leu Ile Asn Pro Ile
290 295 300

Leu Tyr Ala Leu Leu Gly His Asp Phe Leu Gln Arg Met Arg Gln Cys
305 310 315 320

Phe Arg Gly Gln Leu Leu Asp Arg Arg Ala Phe Leu Arg Ser Gln Gln
325 330 335

Asn Gln Arg Ala Thr Ala Glu Thr Asn Leu Ala Ala Gly Asn Asn Ser
340 345 350

Gln Ser Val Ala Thr Ser Leu Asp Thr Asn Ser Lys Asn Tyr Asn Gln
355 360 365

His Ala Lys Arg Ser Val Ser Phe Asn Phe Pro Ser Gly Thr Trp Lys
370 375 380

Gly Gly Gln Lys Thr Ala Ser Asn Asp Thr Ser Thr Lys Ile Pro His
385 390 395 400

Arg Leu Ser Gln Ser His His Asn Leu Ser Gly Val
405 410

<210> 23
<211> 990
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 homolog
(rhUL33)

<220>
<221> CDS
<222> (1)..(990)
<223> rhUL33

<400> 23
atgaccaatc tttactctgc caatttctc accttgcata tacttccttt tatacgtttta 60
agaatcaac accttttacc tgccagtgc aatttctctc cctgttgc 120
tactctagct gcagcgtagg ttttgcata gttgcactga tagcggccga ccgataccga 180
gtgattcattc gcccgaactca agctcgccaa tccttaccgtt acacatataat gatagttaggc 240
ttaacgtggc tcattggctt gatctgcgtt acccccgggg gggtctacac aaccattgtt 300
gctcaccgcg atgggaaag tgatgctcaa agacacaata cttgcattat gcaacttgcg 360
tatgtatgaag tttacgtcctt catggtctgg aaacttctca tcgttttagt ctggggcata 420
gtgccagtttgc tcatgtatgag ctgggttttac gcgtttttt acaataactgt acaaagaaca 480
gccaaaaaaac aacaacgtac gttgaaattc gtaaaggat tttacacgtt atgcccaccgtt aggatggccg 540
atccaaactc cctatgtgtc aatcatgatt ttaacacgtt atgcccaccgtt aggatggccg 600
atggaatgcg ccgatctaact tagacgcgcg gtcataaca cgtttttcccg ttcgtcccc 660
aatctacatt gcatggtcaa ccccatcctc tacgtctca tgggaaatga ctttgtgtct 720
aaagtggcc aatgcttcg gggggaaactc acgaaccgtc gaactttct gcgttccaag 780
caacaagccc gcaactcgga cgatgtaccg acaattgtca gtcaacaacc cggcacacc 840
accatcgta ataagcccga aaaaaaccccg cacgtaaaac gcggtgtatc ttcagcgctc 900
agcgcatctt ccgaactcgca agcggccaaa aaagccaaag acaaagccaa gcggtttcc 960
atgtcccacc aaaacctacg tctgacgtga 990

<210> 24
<211> 329
<212> PRT
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 homolog
(rhUL33)

<400> 24
Met Thr Asn Leu Tyr Ser Ala Asn Phe Leu Thr Leu Ile Val Leu Pro
1 5 10 15

Phe Ile Val Leu Ser Asn Gln His Leu Leu Pro Ala Ser Ala Val Thr
20 25 30

Cys Lys Phe Leu Ser Leu Leu Tyr Tyr Ser Ser Cys Ser Val Gly Phe
35 40 45

Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Ile His Arg
50 55 60

Arg Thr Gln Ala Arg Gln Ser Tyr Arg Asn Thr Tyr Met Ile Val Gly
65 70 75 80

Leu Thr Trp Leu Ile Gly Leu Ile Cys Ala Thr Pro Gly Gly Val Tyr
85 90 95

Thr Thr Ile Val Ala His Arg Asp Gly Glu Ser Asp Ala Gln Arg His
 100 105 110
 Asn Thr Cys Ile Met His Phe Ala Tyr Asp Glu Val Tyr Val Leu Met
 115 120 125
 Val Trp Lys Leu Leu Ile Val Leu Val Trp Gly Ile Val Pro Val Val
 130 135 140
 Met Met Ser Trp Phe Tyr Ala Phe Phe Tyr Asn Thr Val Gln Arg Thr
 145 150 155 160
 Ala Lys Lys Gln Gln Arg Thr Leu Lys Phe Val Lys Val Leu Leu
 165 170 175
 Ser Phe Ile Ile Ile Gln Thr Pro Tyr Val Ser Ile Met Ile Phe Asn
 180 185 190
 Thr Tyr Ala Thr Val Gly Trp Pro Met Glu Cys Ala Asp Leu Thr Arg
 195 200 205
 Arg Arg Val Ile Asn Thr Phe Ser Arg Leu Val Pro Asn Leu His Cys
 210 215 220
 Met Val Asn Pro Ile Leu Tyr Ala Leu Met Gly Asn Asp Phe Val Ser
 225 230 235 240
 Lys Val Gly Gln Cys Phe Arg Gly Glu Leu Thr Asn Arg Arg Thr Phe
 245 250 255
 Leu Arg Ser Lys Gln Gln Ala Arg Asn Ser Asp Asp Val Pro Thr Ile
 260 265 270
 Val Ser Gln Gln Pro Ala Thr Pro Thr Ile Val Asn Lys Pro Glu Lys
 275 280 285
 Asn Pro His Val Lys Arg Gly Val Ser Phe Ser Val Ser Ala Ser Ser
 290 295 300
 Glu Leu Ala Ala Ala Lys Lys Ala Lys Asp Lys Ala Lys Arg Leu Ser
 305 310 315 320
 Met Ser His Gln Asn Leu Arg Leu Thr
 325

<210> 25
 <211> 1328
 <212> DNA
 <213> Rhesus cytomegalovirus

 <220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
 variant homolog (rhUL33 spliced)

 <220>
 <221> CDS
 <222> (1)..(1328)
 <223> rhUL33 spliced

<400> 25
 atggcagtca ctttacgagg cggcagcccc ataaaacttta aactcatgat tgcagccac 60
 agaaaaccgga aatttcacga gatacggctg tttagcgtt ctgctatccg tccaggcggg 120
 ttatggaaac cattttcac aaccgaacga gtgaaaactaa ttccatattt cacatcaaca 180
 ccacctgcaa tgtgaccgac tcactgtacg ccgcggaaact aggcgaagcc ctcgtgaaca 240
 ggcgcgtacg tttatccgt accccctca acggccatcg cctcgtcaca cagctattgg 300
 ccaaccgagt tcatggatac tccaccccgta ttatctacat gaccaatctt tactctgcca 360
 attttctcac cttgatagta cttccttttac tcgttttaag caatcaacac cttttacctg 420
 ccagtgcagt aacctgtaaa tttctctccc tgggttacta ctctagctgc agcgttaggt 480
 ttgctacagt ggcactgata gggccgacc gataccgagt gattcategc cgaactcaag 540
 ctcgccaatc ctaccgtaa acatataatgatg tagtaggctt aacgtggctc attggcttga 600
 tctgcgtac cccccgggggg gtctacacaa ccattgttagc tcaccgcgt gggggaaagtg 660
 atgctcaaaag acacaataact tgcattatgc actttgcgtt tgatgaagtt tacgtcctca 720
 tggctctggaa acttctcata gtttttagtct gggcatagt ggcagttgtc atgatgagct 780
 gtttttacgc gttttttac aatactgtac aaagaacagc caaaaaacaa caacgtacgt 840
 tgaattcgt aaaggattta ctcctgtcat tcatacatcat ccaaactccc tatgtgtcaa 900
 tcatgattt taacacgtat gcccacgtat gatggccgtat ggaatgcgc gatctaacta 960
 gacgcccgtat catcaacacg tttcccgatc tcgtccccaa tctacattgc atggtaacc 1020
 ccatcctcta cgctctcatg gaaaatgact ttgtgtctaa agtggccaa tgctttcggg 1080
 gggaaactcac gaaccgtcga actttctgc gttccaagca acaagccgc aactcggacg 1140
 atgtaccgac aattgtcagt caacaacccg ccacacccac catcgtcaat aagcccgaaa 1200
 aaaacccgcgatcgtaaaacgc ggtgtatctt tcagcgtcag cgcatttcc gaactcgcag 1260
 cggccaaaaaa agccaaagac aaagccaagc ggcttccat gtcccaccaa aacctacgtc 1320
 tgacgtga 1328

<210> 26
 <211> 441
 <212> PRT
 <213> Rhesus cytomegalovirus

<220>
 <223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
 variant homolog (rhUL33 spliced)

<400> 26
 Met Ala Val Thr Leu Arg Gly Gly Ser Pro Ile Asn Phe Lys Leu Met
 1 5 10 15

Ile Val Ser His Arg Asn Arg Lys Phe His Glu Ile Arg Leu Phe Gln
 20 25 30

Arg Ser Ala Ile Arg Pro Gly Gly Leu Trp Lys Pro Phe Phe Thr Thr
 35 40 45

Glu Arg Glu Thr Asn Ser Ile Leu His Ile Asn Thr Thr Cys Asn Val
 50 55 60

Thr Asp Ser Leu Tyr Ala Ala Lys Leu Gly Glu Ala Leu Val Asn Ser
 65 70 75 80

Ala Leu Ala Leu Phe Gly Thr Pro Leu Asn Ala Ile Val Leu Val Thr
 85 90 95

Gln Leu Leu Ala Asn Arg Val His Gly Tyr Ser Thr Pro Ile Ile Tyr
 100 105 110

Met Thr Asn Leu Tyr Ser Ala Asn Phe Leu Thr Leu Ile Val Leu Pro
 115 120 125

Phe Ile Val Leu Ser Asn Gln His Leu Leu Pro Ala Ser Ala Val Thr
 130 135 140

 Cys Lys Phe Leu Ser Leu Leu Tyr Tyr Ser Ser Cys Ser Val Gly Phe
 145 150 155 160

 Ala Thr Val Ala Leu Ile Ala Ala Asp Arg Tyr Arg Val Ile His Arg
 165 170 175

 Arg Thr Gln Ala Arg Gln Ser Tyr Arg Asn Thr Tyr Met Ile Val Gly
 180 185 190

 Leu Thr Trp Leu Ile Gly Leu Ile Cys Ala Thr Pro Gly Gly Val Tyr
 195 200 205

 Thr Thr Ile Val Ala His Arg Asp Gly Glu Ser Asp Ala Gln Arg His
 210 215 220

 Asn Thr Cys Ile Met His Phe Ala Tyr Asp Glu Val Tyr Val Leu Met
 225 230 235 240

 Val Trp Lys Leu Leu Ile Val Leu Val Trp Gly Ile Val Pro Val Val
 245 250 255

 Met Met Ser Trp Phe Tyr Ala Phe Phe Tyr Asn Thr Val Gln Arg Thr
 260 265 270

 Ala Lys Lys Gln Gln Arg Thr Leu Lys Phe Val Lys Val Leu Leu Leu
 275 280 285

 Ser Phe Ile Ile Ile Gln Thr Pro Tyr Val Ser Ile Met Ile Phe Asn
 290 295 300

 Thr Tyr Ala Thr Val Gly Trp Pro Met Glu Cys Ala Asp Leu Thr Arg
 305 310 315 320

 Arg Arg Val Ile Asn Thr Phe Ser Arg Leu Val Pro Asn Leu His Cys
 325 330 335

 Met Val Asn Pro Ile Leu Tyr Ala Leu Met Gly Asn Asp Phe Val Ser
 340 345 350

 Lys Val Gly Gln Cys Phe Arg Gly Glu Leu Thr Asn Arg Arg Thr Phe
 355 360 365

 Leu Arg Ser Lys Gln Gln Ala Arg Asn Ser Asp Asp Val Pro Thr Ile
 370 375 380

 Val Ser Gln Gln Pro Ala Thr Pro Thr Ile Val Asn Lys Pro Glu Lys
 385 390 395 400

 Asn Pro His Val Lys Arg Gly Val Ser Phe Ser Val Ser Ala Ser Ser
 405 410 415

 Glu Leu Ala Ala Ala Lys Lys Ala Lys Asp Lys Ala Lys Arg Leu Ser
 420 425 430

 Met Ser His Gln Asn Leu Arg Leu Thr
 435 440

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<210> 27
<211> 2100
<212> DNA
<213> Rhesus cytomegalovirus

<220>
<223> rhesus monkey cytomegalovirus (rhCMV) UL33 splice
      variant homolog (rhUL33 spliced) nucleotide
      sequence segment that extends 1000 nucleotides
      upstream and downstream of the rhUL33 reading
      frame

<220>
<221> exon
<222> (603) .. (752)
<223> exon 1

<220>
<221> intron
<222> (753) .. (830)

<220>
<221> exon
<222> (831) .. (2006)
<223> exon 2

<220>
<221> misc_feature
<222> (1017) .. (2006)
<223> unspliced gene

<400> 27
cgcccaagat gttctgacat gaacaatcac ttttccgaga tagatgagtt 60
tggtagggc atttaccaga gaactattgg agtgcgcgc aagatgaagc ttcactggcc 120
gtatttcgaa catattgtt gatatacgta gtaaagaatc ttctaaagcc atgacgtctt 180
tctgacgaag ttgaataaaat tctatctcac cagtagccaa aggctgacac tcagacaact 240
ttgccaaggc cgttgcaccc accatggcat tctgaatcac agtaacatcc gtccgagaat 300
cgtcacccaa aacgggtggcc tccaaagttc gcaggtgagg ccgagcctt actggatctc 360
gaaagggata catgtgtgct cgccgagtga cagcattagc attaacctca aactcatcta 420
aaagcgatga taaatcagga atatgatagc gcaattctcg atagtaggaa aaccagagga 480
ctaattgggtt gaacagacag ctccgtctgt gcaaaaaactt ttccgcgtt tttctgagaa 540
ttttaggatg ctgctctaaa tctacgttct ctttagtcgg cagggtctt aaaaagttag 600
tgcgtggcact cactttacga ggcggcagcc cgataaaactt taaactcatg attgtcagcc 660
acagaaaccg gaaatttcac gagatacggc tggttcagcg ttctgcatac cgccaggcg 720
ggttatggaa accattcttc acaaccgaac ggtgagtgac atttaagaca gtttaatagc 780
caacactcgt aacgtctcgaa aagctgataa gtttcgttt tccacagagt gaaaactaatt 840
ccattttgcg catcaacacc acctgcatacg tgaccgactc actgtacgccc gccaaactag 900
gccaaggccct cgtgaacagc ggcgttagctt tattcggtac cccccctcaac gccatcggtcc 960
tcgtcacaca gctattggcc aaccgagttc atggataactc caccggatt atctacatga 1020
ccaatcttta ctctgccaat tttctcacct tgatagttact tccttttatac gttttaagca 1080
atcaacaccc tttacactgccc agtgcagtaa cctgtaaatt tctctccctg ttgtactact 1140
ctagctgcag cgttaggtttt gctacagttt cactgatagc ggcggaccga taccgagtga 1200
ttcatacgccg aactcaagct cgccaaatcc accgtaaacac atatatgata gtaggcttaa 1260
cgtggctcat tggcttgatc tgcgttaccc cgggggggtt ctacacaacc attgtagctc 1320
accgcgatgg ggaaagtgtat gctcaaagac acaataacttg cattatgcac ttgcgtatg 1380
atgaagttt cgtccctcatg gtctggaaac ttctcatcg ttttagtctgg ggcatagtgc 1440
cagttgtcat gatgagctgg ttttacgcgt ttttttacaa tactgtacaa agaacagcca 1500
aaaaacaaca acgtacgttg aaattcgtaa aggtattact cctgtcattc atcatcatcc 1560
aaactcccta tgtgtcaatc atgatttta acacgtatgc caccgttagga tggccgatgg 1620
aatgcgccga tcttaactaga cgccgagtca tcaacacgtt ttcccgctc gttccccaaatc 1680
tacattgtcat ggtcaaccccc atcctctacg ctctcatggg aaatgactttt gtgtctaaag 1740

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tgggccaatg ctttcggggg gaactcacga accgtcgAAC ttttctgcgt tccaagcaac 1800
aagccccgcaa ctcggacgat gtaccgacaa ttgtcagtca acaaccggcc acacccacca 1860
tcgtcaataa gccccaaaaa aacccgcacg taaaacgcgg tgtatcttc agcgtcagcg 1920
catcttccga actcgcagcg gccaaaaaaag ccaaagacaa agccaagcgg ctttccatgt 1980
cccacccaaa cctacgtctg acgtgaattt tccttagaggc tgcctccacg ggtttacata 2040
catatctcgG tacttgctac acttgatcac tttactgcgg acaccacggc caatgcac 2100

<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.1 amplification primer sequence (upper
strand)

<400> 28
tatgaataac acatcttgca acttc

25

<210> 29
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.1 amplification primer sequence (lower
strand)

<400> 29
cacacagacc acatgtac

18

<210> 30
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.2 amplification primer sequence (upper
strand)

<400> 30
attcaacatg accaacgcgg g

21

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.2 amplification primer sequence (lower
strand)

<400> 31
gcatttccgt ggattcg 17

<210> 32
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.3 amplification primer sequence (upper
strand)

<400> 32
catgaccaac actaac 16

<210> 33
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.3 amplification primer sequence (lower
strand)

<400> 33
gagtcttttg tgagcc 16

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.4 amplification primer sequence (upper
strand)

<400> 34
tatgaattcg agccagcac 19

<210> 35
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.4 amplification primer sequence (lower
strand)

<400> 35
gtacgcgact aagacagag 19

<210> 36
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.5 amplification primer sequence (upper
strand)

<400> 36
aaagatgact accaccac 18

<210> 37
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUS28.5 amplification primer sequence (lower
strand)

<400> 37
ataaaccttagc acctccccc 18

<210> 38
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUL78 amplification primer sequence (upper
strand)

<400> 38
ctgaaaaccat gattacgg 18

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUL78 amplification primer sequence (lower
strand)

<400> 39
cacgcagcac aagagcac 18

<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUL33 amplification primer sequence (upper
strand)

<400> 40
catgaccaat ctttactc

18

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUL33 amplification primer sequence (lower
strand)

<400> 41
gtgtcgccac tcctaccc

18

<210> 42
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUL33 splice amplification primer sequence (upper
strand)

<400> 42
aagtttagtga tggcagtc

18

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:rhUS28 homolog
rhUL33 splice amplification primer sequence (lower
strand)

<400> 43
gtatgtaaac ccgtggag

18

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 44
gccaatgcat cctctggatg tattgtga

28

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 45
tgcttgggaa atctctgcac

20

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 46
cccttcctga ctactaatgt ac

22

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested PCR CMV
specific primer able to amplify the rhCMV
immediate early 2 gene

<400> 47
ttggggaaatc tctgcacaag

20

<210> 48
<211> 354
<212> PRT
<213> Human cytomegalovirus

<220>
<223> human cytomegalovirus (HCMV) AD169 strain open
reading frame US28

<400> 48
Met Thr Pro Thr Thr Thr Ala Glu Leu Thr Thr Glu Phe Asp Tyr
1 5 10 15

Asp Glu Asp Ala Thr Pro Cys Val Phe Thr Asp Val Leu Asn Gln Ser
20 25 30

Lys Pro Val Thr Leu Phe Leu Tyr Gly Val Val Phe Leu Phe Gly Ser
 35 40 45

Ile Gly Asn Phe Leu Val Ile Phe Thr Ile Thr Trp Arg Arg Arg Ile
 50 55 60

Gln Cys Ser Gly Asp Val Tyr Phe Ile Asn Leu Ala Ala Ala Asp Leu
 65 70 75 80

Leu Phe Val Cys Thr Leu Pro Leu Trp Met Gln Tyr Leu Leu Asp His
 85 90 95

Asn Ser Leu Ala Ser Val Pro Cys Thr Leu Leu Thr Ala Cys Phe Tyr
 100 105 110

Val Ala Met Phe Ala Ser Leu Cys Phe Ile Thr Glu Ile Ala Leu Asp
 115 120 125

Arg Tyr Tyr Ala Ile Val Tyr Met Arg Tyr Arg Pro Val Lys Gln Ala
 130 135 140

Cys Leu Phe Ser Ile Phe Trp Trp Ile Phe Ala Val Ile Ile Ala Ile
 145 150 155 160

Pro His Phe Met Val Val Thr Lys Lys Asp Asn Gln Cys Met Thr Asp
 165 170 175

Tyr Asp Tyr Leu Glu Val Ser Tyr Pro Ile Ile Leu Asn Val Glu Leu
 180 185 190

Met Leu Gly Ala Phe Val Ile Pro Leu Ser Val Ile Ser Tyr Cys Tyr
 195 200 205

Tyr Arg Ile Ser Arg Ile Val Ala Val Ser Gln Ser Arg His Lys Gly
 210 215 220

Arg Ile Val Arg Val Leu Ile Ala Val Val Leu Val Phe Ile Ile Phe
 225 230 235 240

Trp Leu Pro Tyr His Leu Thr Leu Phe Val Asp Thr Leu Lys Leu Leu
 245 250 255

Lys Trp Ile Ser Ser Cys Glu Phe Glu Arg Ser Leu Lys Arg Ala
 260 265 270

Leu Ile Leu Thr Glu Ser Leu Ala Phe Cys His Cys Cys Leu Asn Pro
 275 280 285

Leu Leu Tyr Val Phe Val Gly Thr Lys Phe Arg Gln Glu Leu His Cys
 290 295 300

Leu Leu Ala Glu Phe Arg Gln Arg Leu Phe Ser Arg Asp Val Ser Trp
 305 310 315 320

Tyr His Ser Met Ser Phe Ser Arg Arg Ser Ser Pro Ser Arg Arg Glu
 325 330 335

Thr Ser Ser Asp Thr Leu Ser Asp Glu Val Cys Arg Val Ser Gln Ile
 340 345 350

Ile Pro